



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/674 195A

Source: PCT

Date Processed by STIC: 09/18/2001

BEST AVAILABLE COPY

ST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/674 195A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,195A

DATE: 09/18/2001

TIME: 13:30:00

Input Set : A:\14014.0325U2.TXT

Output Set: N:\CRF3\09182001\I674195A.raw

4 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS
 5 REPRESENTED BY THE
 6 SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
 7 CENTERS FOR
 8 DISEASE CONTROL AND PREVENTION
 9 Rosely M. Zancopé-Oliveira
 10 Timothy J. Lott
 11 Leonard W. Mayer
 12 Errol Reiss
 13 George S. Deepe

Does Not Comply
 Corrected Diskette Needed

See Page 5 and 7

17 <120> TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
 18 HISTOPLASMA CAPSULATUM, ANTIGENS, VACCINES, AND ANTIBODIES,
 19 METHODS AND KITS FOR DETECTING HISTOPLASMOSIS

22 <130> FILE REFERENCE: 14114.0325U2

24 <140> CURRENT APPLICATION NUMBER: 09/674,195A

25 <141> CURRENT FILING DATE: 2000-10-26

27 <150> PRIOR APPLICATION NUMBER: 60/083,676

28 <151> PRIOR FILING DATE: 1998-04-30

30 <150> PRIOR APPLICATION NUMBER: PCT/US99/09151

31 <151> PRIOR FILING DATE: 1999-04-27

33 <160> NUMBER OF SEQ ID NOS: 13

35 <170> SOFTWARE: FastSEQ for Windows Version 4.0

37 <210> SEQ ID NO: 1

38 <211> LENGTH: 3862

39 <212> TYPE: DNA

40 <213> ORGANISM: Histoplasma capsulatum

42 <220> FEATURE:

43 <221> NAME/KEY: misc_feature

44 <222> LOCATION: (1)...(3862) OK

45 <223> OTHER INFORMATION: n = a,t,c, or g

47 <400> SEQUENCE: 1

48	ggatcctgct	ggctccgata	actttgcttt	atccaagggt	ctcggcggaat	gccaggtgcc	60
49	atcgatctat	atcttggaagt	ttatcacctc	aatggcttca	ccccatgacg	caccttttat	120
50	ttttattttc	attcatcttc	tctgtggcaa	acatgcaggt	atgcgagctc	tggaccctgg	180
51	ggtgtggccc	ttgatgcata	tggtttattt	atagccgccc	ggaagccctg	gcctgttaaa	240
52	ttttggacct	cctcccgcga	ttctttccaa	acttcgtgcg	tccgtttccc	atttcccccc	300
53	tccccatttg	ggttccttat	aggccactgc	gtgctccact	caagaagggt	cccagtcatt	360
54	ttggtcccta	ccctctccaa	cactatctgc	atatgtaata	tatatcgata	tctaactgcc	420
55	attgattatt	tgtcttcttc	agcatctttt	tgtctcgagc	aagcttactc	cacgttcaat	480
56	tcagggggta	aaaatgcggt	cgctcaagct	tatactcgcc	tcggcggtg	ttgtttctgc	540
57	agcctgtccc	tacatgtcag	gggagatgcc	tagcggtcag	aaaggccccc	tcgatcgccg	600
58	ccatgacact	ctctccgacc	ctacggacca	gtttcttagc	aagttttaca	ttgacgatga	660
59	acagtcggtg	ctaacaacgg	acgtgggtgg	tcccatcgag	gaccaacaca	gcctgaaggc	720
60	tggaaataga	ggcccaactc	tacttgagga	ttttatcttc	cgccagaaga	ttcaaacatt	780
61	tgatcatgag	agggtatgta	gatacaaaat	atgtgaccgt	gttgcaaata	cgctaattca	840
62	attttacgca	ggttcctgag	cgcgcgctcc	atgctcgagg	agctggtgcc	catggcggtat	900
63	tcacatccta	taataactgg	tcgaatatca	cagccgcata	cttcttgaac	gcggcaggaa	960

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Input Set : A:\14014.0325U2.TXT

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64 agcagacacc agtattcgtg cggttttcta cagtcgctgg tagcagaggc agtggtgact 1020
65 ctgctcgcga tatccacgga tttgcgaccc gtctgtatac cgatgaaggc aattttggta 1080
66 agcattatat cgtggtagtc atactcataa cagcacaaca aatatgaata caaaccagg 1140
67 acctaggctg actactcggc aatgtagata tcgtcggaaa caacgttcca gtcttcttca 1200
68 ttcaggacgc tattcaattc cctgatttga ttcacgctgt caagccgcaa ccagacagt 1260
69 aaattcccca ggcgtcaact gcacatgata cggcatggga tttcctcagc cagcagcca 1320
70 gctcattgca tgccctcttc tgggcaatgt caggacatgg aatccctcgc tcaatgcgtc 1380
71 atggtgatgg gtggggcgtc cataccttcc gacttgtcac cgacgagggc aactcgacct 1440
72 tggccaagtt tcgtggaag accctccaag gaagagcggg cctgggtatgg gaagaggcac 1500
73 aggcctcttg cggaaagaat cccgacttcc atcgacaaga cctctgggat gccattgaat 1560
74 ctggaaggta ccctgagtg gaggtaagat atgattcccc caaatcatta gttctgacag 1620
75 tgtttctctg ctctgctcgg tgccttttct gtctttttct atatcttcaa ctaagactga 1680
76 ctttatatac gttttactca tatacctggg ctttcaattg gtgaatgaag cagatcaatc 1740
77 caagtttgat ttcgatctat tagatcccac caaaatcacc ccagaagaac ttgttccttt 1800
78 caccccaatc ggaaaaatgg tcttgaacgg aaacccaaaa agttattttg ccgaaactga 1860
79 gcagatcatg gttggtccac cccctatata tttggaatat gaatacatgt atagctagat 1920
80 gaagcgtata tctaaatata tttccacagt tccaaccagg tcatgtagtt cgcggaatcg 1980
81 atttccagga tgaccctttg cttcaggggc gcttgtactc ctaccttgac actcaattga 2040
82 atcgccatgg aggtcccaac ttcgagcaac tgccgatcaa cagaccccg c atccattcc 2100
83 ataacaacaa tcgcgacggt gctggtaagc taattctcac ctaccatgtc aacttccatc 2160
84 ttgaccaat cgatttgat agagtattaa catccccgtc tgcacaggac aaatgttcat 2220
85 cctctaaac acggccgcat atacacccaa ctcaatgagc aacggattcc cacaacaagc 2280
86 caaccggacc cataacagag gattcttcac cgcacctggg cgtatggtaa atggaccact 2340
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90 cctcgccgc cgcgctcgcc tagctatcgg cgtogaaccc ccatccccgg acccaacctt 2580
91 ctaccacaac aaggcaaccg tccccatcgg caccttcggc acgaatctcc tgcggctcga 2640
92 cgggctgaaa atcgccctcc tgacaagaga cgacggtagc ttcacgatcg cggagcagct 2700
93 ccgggcccgc tttaacagcg ccaacaacaa agtagatac gtccatagtg gctcatcgt 2760
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100 aggtttgggg cgcaaatatg ggtttactac ccccccccc cccttttttt ttttctttt 3180
101 ctgtttttcc atctttggtt gaggtaatat tgcagatac agtaaattgc gtttacgaaa 3240
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103 gtgtaactat aataatttat aataactaat aacttataat taatgtctat tgtaatttcc 3360
104 tctcacattc aatctatatt tgatccttgt cctttgtagc tgtttaaata taagccaaga 3420
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110 atagataaaa cctgaacgat ttaggccctg ttgggggaaa taggggttag gggggcgagc 3780
111 tacatatcat tcccatatga ccaaaaacta aaatagatat atatatatat atatatatat 3840
112 acaacacctt caaaaaggat cc 3862

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DATE: 09/18/2001

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Input Set : A:\14014.0325U2.TXT

Output Set: N:\CRF3\09182001\I674195A.raw

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114 <210> SEQ ID NO: 2
115 <211> LENGTH: 707
116 <212> TYPE: PRT
117 <213> ORGANISM: Histoplasma capsulatum
119 <400> SEQUENCE: 2
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121 1 5 10 15
122 Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
123 20 25 30
124 Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
125 35 40 45
126 Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
127 50 55 60
128 Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
129 65 70 75 80
130 Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
131 85 90 95
132 Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
133 100 105 110
134 Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
135 115 120 125
136 Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
137 130 135 140
138 Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
139 145 150 155 160
140 Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
141 165 170 175
142 Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
143 180 185 190
144 Thr Ala Trp Asp Phe Leu Ser Gln Pro Ser Ser Leu His Ala Leu
145 195 200 205
146 Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
147 210 215 220
148 Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
149 225 230 235 240
150 Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
151 245 250 255
152 Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
153 260 265 270
154 His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
155 275 280 285
156 Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
157 290 295 300
158 Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
159 305 310 315 320
160 Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
161 325 330 335
162 Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
163 340 345 350

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Input Set : A:\14014.0325U2.TXT

Output Set: N:\CRF3\09182001\I674195A.raw

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164 Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
165          355          360          365
166 Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
167          370          375          380
168 Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
169 385          390          395          400
170 Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr
171          405          410          415
172 Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His
173          420          425          430
174 Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
175          435          440          445
176 Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
177          450          455          460
178 Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
179 465          470          475          480
180 Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
181          485          490          495
182 Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
183          500          505          510
184 Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
185          515          520          525
186 Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
187          530          535          540
188 Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
189 545          550          555          560
190 Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
191          565          570          575
192 Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
193          580          585          590
194 Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
195          595          600          605
196 Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
197          610          615          620
198 Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
199 625          630          635          640
200 Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
201          645          650          655
202 Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
203          660          665          670
204 Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
205          675          680          685
206 Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg
207          690          695          700
208 Ser Leu Val
209 705
211 <210> SEQ ID NO: 3
212 <211> LENGTH: 8
213 <212> TYPE: PRT

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RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/674,195A

TIME: 13:30:01

Input Set : A:\14014.0325U2.TXT

Output Set: N:\CRF3\09182001\I674195A.raw

214 <213> ORGANISM: Histoplasma capsulatum
 216 <400> SEQUENCE: 3
 217 Ser Asp Pro Thr Asp Gln Phe Leu
 218 1 5
 220 <210> SEQ ID NO: 4
 221 <211> LENGTH: 15
 222 <212> TYPE: PRT
 223 <213> ORGANISM: Histoplasma capsulatum
 225 <400> SEQUENCE: 4
 226 Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
 227 1 5 10 15
 229 <210> SEQ ID NO: 5
 230 <211> LENGTH: 9
 231 <212> TYPE: PRT
 232 <213> ORGANISM: Histoplasma capsulatum
 234 <400> SEQUENCE: 5
 235 Thr Leu Gln Gly Arg Ala Gly Leu Val
 236 1 5
 238 <210> SEQ ID NO: 6
 239 <211> LENGTH: 16
 240 <212> TYPE: PRT
 241 <213> ORGANISM: Histoplasma capsulatum
 243 <400> SEQUENCE: 6
 244 Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
 245 1 5 10 15
 247 <210> SEQ ID NO: 7
 248 <211> LENGTH: 6
 249 <212> TYPE: PRT
 250 <213> ORGANISM: Histoplasma capsulatum
 252 <400> SEQUENCE: 7
 253 Ser Gly Arg Tyr Pro Glu
 254 1 5
 256 <210> SEQ ID NO: 8
 257 <211> LENGTH: 10
 258 <212> TYPE: PRT
 259 <213> ORGANISM: Histoplasma capsulatum
 261 <400> SEQUENCE: 8
 262 Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
 263 1 5 10
 265 <210> SEQ ID NO: 9
 266 <211> LENGTH: 14
 267 <212> TYPE: PRT
 268 <213> ORGANISM: Unknown
 W--> 270 <220> FEATURE:
 W--> 270 <223> OTHER INFORMATION:
 270 <400> SEQUENCE: 9
 271 Ile Ile Pro Glu Leu Val Pro Phe Thr Pro Ile Gly Lys
 272 1 5 10
 274 <210> SEQ ID NO: 10

A 213 response of Unknown Requires an
 explanation or description in field
 223.

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

DATE: 09/18/2001

PATENT APPLICATION: US/09/674,195A

TIME: 13:30:02

Input Set : A:\14014.0325U2.TXT

Output Set: N:\CRF3\09182001\I674195A.raw

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:270 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:270 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:279 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:279 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:300 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:300 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:308 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:308 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: